

ATTORNEY DOCKET NO. 14028.0295P1

SEQUENCE LISTING

<110> The Government of the United States of America, as represented by t
Secretary, Department of Health and Human Services

NEVILLE, David
WOO, Jung-Hee
LIU, Yuan-Yi

<120> METHODS FOR EXPRESSION AND PURIFICATION
OF IMMUNOTOXINS

<130> 14028.0295P1

<140> Unassigned

<141> 2004-08-02

<150> 60/491,923

<151> 2003-08-01

<160> 35

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 22

<212> PRT

<213> H. sapiens

<400> 1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Thr | Leu | His | Ala | Asp | Ala | Ile | His | Arg | Gly | Gly | Gly | Gln | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Pro | Thr | Ala | Arg | Arg | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

<210> 2

<211> 22

<212> PRT

<213> M. musculus

<400> 2

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Thr | Leu | His | Ala | Asp | Ala | Ile | His | Arg | Gly | Gly | Gly | Gln | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Pro | Thr | Ala | Arg | Arg | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

<210> 3

<211> 22

<212> PRT

<213> R. norvegicus

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<400> 3

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile
1 5 10 15
Ile Pro Thr Ala Arg Arg
20

<210> 4

<211> 22

<212> PRT

<213> C. griseus

<400> 4

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile
1 5 10 15
Ile Pro Thr Ala Arg Arg
20

<210> 5

<211> 22

<212> PRT

<213> D. melanogaster

<400> 5

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile
1 5 10 15
Ile Pro Thr Thr Arg Arg
20

<210> 6

<211> 22

<212> PRT

<213> C. elegans

<400> 6

Asp Val Thr Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile
1 5 10 15
Ile Pro Thr Ala Arg Arg
20

<210> 7

<211> 22

<212> PRT

<213> S. pombe

<400> 7

Asp Val Val Leu His Ala Asp Ala Ile His Arg Gly Gly Gly Gln Ile
1 5 10 15
Ile Pro Thr Ala Arg Arg
20

<210> 8

<211> 22

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<212> PRT

<213> P. pastoris

<400> 8

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Thr | Leu | His | Ala | Asp | Ala | Ile | His | Arg | Gly | Gly | Gly | Gln | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Pro | Thr | Met | Lys | Arg | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

<210> 9

<211> 22

<212> PRT

<213> S. cerevisiae

<400> 9

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Thr | Leu | His | Ala | Asp | Ala | Ile | His | Arg | Gly | Gly | Gly | Gln | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ile | Pro | Thr | Met | Arg | Arg | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

<210> 10

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| gatgttaccc | tgcacgccga | tgctatccac | cgccgcggag | gacaagtcac | tccaaccatg | 60 |
| aagaga | | | | | | 66 |

<210> 11

<211> 223

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| actttgaagt | tcttaatttt | gttcctcgta | gaaagaacgc | atagataatt | caaaatggca | 60 |
| aaatgggtat | gtgttttttt | atagttcatg | tgccgaacaa | ctaccgtttt | aacttcactg | 120 |
| tcgatcagat | gcgatccctt | atggacaagg | tgtccaacgt | ccgtaacatg | tcggttattg | 180 |
| cccacgttga | tcacggttaag | tccactttaa | ctgactccct | ggt | | 223 |

<210> 12

<211> 250

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| acttttgaagt | tcttaatttt | gttcctcgta | gaaagaacgc | atagataatt | caaaatgggt | 60 |
| atgtgttttt | ttatagttca | tgtgccgaac | aactaccgtt | tcaagatggg | agccagccac | 120 |
| taacatctcc | tctagttaac | ttcactgtcg | atcagatgcg | atcccttatg | gacaagggtga | 180 |
| ccaacgtccg | taacatgtcg | gttattgccc | acgttgatca | cggtaagtcc | actttaactg | 240 |
| actccctggg | | | | | | 250 |

<210> 13

<211> 2601

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| atgggttaact | tcaactgtcga | tcagatgcga | tcccttatgg | acaagggtgac | caacgtccgt | 60 |
| aacatgtcgg | ttattgccc | cgttgatcac | ggtaagtcca | ctttaactga | ctccctgggtg | 120 |
| caacgtgccg | gtattatttc | tgtgccgaag | gctgggtgagg | cccgtttcac | tgataactaga | 180 |
| aaggacgagc | aagagagagg | tatcaccatc | aagtctaccg | ccatttcttt | gtactctgag | 240 |
| atgggtgacg | acgatgtcaa | ggagatcaag | cagaagactg | aaggtaacag | tttccttatc | 300 |
| aacttaattg | actccccagg | tcacgttgac | ttctcttctg | aggtcactgc | tgctctgctg | 360 |
| gttactgacg | gtgctttggg | cgtcgttgac | tgtgttgaag | gtgtctgtgt | tcaaaactgag | 420 |
| accgttttgc | gtcaagcttt | gggtgaaaga | atcaagccag | ttgttgtcat | taacaaggtc | 480 |
| gaccgtgctc | ttttggagtt | gcaagttacc | aaggaggacc | tgtaccagtc | tttcgctaga | 540 |
| accgtcgagt | ccgtaaacgt | cgttatcgct | acttacactg | acaagaccat | tggtgacaac | 600 |
| caagtctacc | cagaacaggg | taccgtcgct | ttcgggttcag | gtctgcacgg | atgggctttc | 660 |
| accgttagac | agttcgccac | tagatactcc | aagaagttcg | gtgttgacag | aatcaagatg | 720 |
| atggagcgtc | tgtggggaga | ctcttacttc | aaccctaaaga | ccaagaaatg | gaccaacaag | 780 |
| gacaaggacg | ccgctggaaa | gcctttggag | cgtgccttca | acatgttcgt | tttggaccct | 840 |
| atcttccgtc | tgtttgctgc | catcatgaac | ttcaagaagg | atgaaattcc | agttctgttg | 900 |
| gagaaattgg | agatcaacct | gaagcgtgag | gagaaggagt | tggagggtaa | ggctcttttg | 960 |
| aagggtgtca | tgagaaagtt | cttgccagct | gccgacgctt | tggttgagat | gattgttctt | 1020 |
| caoctgccat | ctccagtcac | cgctcaagct | tacagagccg | agactttgta | cgaagggtcca | 1080 |
| tctgatgacc | aattctgcat | tggtatcaga | gagtgtgacc | ctaaggctga | gctgatgggt | 1140 |
| tacatttcca | agatgggtgcc | aacctccgac | aaaggtagat | tctacgcctt | cggtcgtggt | 1200 |
| ttctccggta | ctgttaagtc | cggtcaaaag | gtcagaatcc | aaggctcctaa | ctacgttcca | 1260 |
| ggtaagaagg | aggacttggt | catcaaggct | gttcaaagaa | ctgttttgat | gatgggaaga | 1320 |
| accgtcgagc | ctattgacga | tgtcccagct | ggtaacattc | tgggtattgt | gggtatcgac | 1380 |
| cagttcttgc | tgaagtctgg | tactcttact | accaacgaag | ccgctcacia | catgaagggtg | 1440 |
| atgaaattct | ctgtctctcc | agttgtgcaa | gttgccggtg | aggtcaagaa | cgctaattgat | 1500 |
| ctgcccagat | tggttgaggg | tctgaagcgt | ttgtccaagt | ctgacctatg | tgtttttaacc | 1560 |
| tacatctccg | agtctgggtga | gcacattggt | gctgggtactg | gtgagctgca | cttggaatc | 1620 |
| tgtttgcaag | atctgcaaga | cgaccacgct | gggtgtccctc | tgaagatttc | tcctccagtt | 1680 |
| gttacctacc | gtgagactgt | cactaacgaa | tcttccatga | ctgccctgtc | caagtctcag | 1740 |
| aacaagcata | acagaattta | cctgaaggct | caaccaattg | acgaggaatt | gtctttgggt | 1800 |
| atcgaagaag | gtaagggttca | cccaagagac | gacttttaaag | ccagagccag | aatcatgggt | 1860 |
| gatgaatacg | gttgggacgt | cactgatgcc | agaaagatct | gggtgttctcg | tccagacggt | 1920 |

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actggtgcc aacttagttgt tgaccagtct aaggctgtcc aatacttgca cgagatcaag 1980
gactctgttg ttgccggttt ccaattggct accaaggaag gtccaatttt gggagaaaac 2040
atgagatccg tcagagtcaa catcttggat gttaccctgc acgccgatgc tatccacaga 2100
ggtggaggac aagtcattcc aaccatgaag agagttacct acgccgcctt cctgttggct 2160
gagccagcta tccaggagcc tatcttcttg gtggagatcc aatgtccaga gaatgccatt 2220
ggtggtatct actctgtttt gaacaagaag agaggtcaag ttatctctga ggaacaaaaga 2280
ccaggtagcc cattgttcac tgtcaaagct tacttgccag ttaacgagtc attcggtttc 2340
accggtgaac tgagacaagc taccgctggt caagctttcc cacagatggt gttcgaccac 2400
tgggccaaaca tgaatggtaa cccattggac ccagcctcca aggtcggtga gattgttctt 2460
gctgccagaa agagacaggg tatgaaggag aacgttcctg gttatgaaga gtactacgac 2520
aagttgtaag cttaatgttt cattaactta tttgtgtcgt tcgtatgtct atttacgtac 2580
ttaattcagt gtattgttgt t 2601

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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14

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Ala His Val Asp His Gly Lys Ser Thr
1             5

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<210> 15

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15

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Asp Glu Gln Glu Arg Gly Ile Thr Ile Lys Ser Thr Ala
1             5             10

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<210> 16

<211> 896

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 16

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Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu
1             5             10             15
Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile
20             25             30

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Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp
 35 40 45
 Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala
 50 55 60
 Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly
 65 70 75 80
 Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys
 85 90 95
 Val Asp Asn Ala Glu Thr Ile Lys Lys Glu Leu Gly Leu Ser Leu Thr
 100 105 110
 Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe Ile Lys Arg Phe
 115 120 125
 Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly
 130 135 140
 Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu
 145 150 155 160
 Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln
 165 170 175
 Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val
 180 185 190
 Arg Arg Ser Val Gly Ser Ser Leu Ser Cys Ile Asn Leu Asp Trp Asp
 195 200 205
 Val Ile Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His
 210 215 220
 Gly Pro Ile Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser
 225 230 235 240
 Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu
 245 250 255
 Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro
 260 265 270
 Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln
 275 280 285
 Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala
 290 295 300
 Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly
 305 310 315 320
 Ala Val His His Asn Thr Glu Glu Ile Val Ala Gln Ser Ile Ala Leu
 325 330 335
 Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val
 340 345 350
 Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu
 355 360 365
 Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly
 370 375 380
 His Lys Thr Gln Pro Phe Leu Pro Trp Asp Ile Gln Met Thr Gln Thr
 385 390 395 400
 Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys
 405 410 415
 Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
 420 425 430
 Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His
 435 440 445
 Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 450 455 460

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| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Thr | Ile | Ser | Asn | Leu | Glu | Gln | Glu | Asp | Ile | Ala | Thr | Tyr | Phe | 465 | 470 | 475 | 480 |
| Cys | Gln | Gln | Gly | Asn | Thr | Leu | Pro | Trp | Thr | Phe | Ala | Gly | Gly | Thr | Lys | 485 | 490 | 495 | |
| Leu | Glu | Ile | Lys | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | 500 | 505 | 510 | |
| Gly | Gly | Ser | Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | 515 | 520 | 525 | |
| Pro | Gly | Ala | Ser | Met | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | Tyr | Ser | Phe | 530 | 535 | 540 | |
| Thr | Gly | Tyr | Thr | Met | Asn | Trp | Val | Lys | Gln | Ser | His | Gly | Lys | Asn | Leu | 545 | 550 | 555 | 560 |
| Glu | Trp | Met | Gly | Leu | Ile | Asn | Pro | Tyr | Lys | Gly | Val | Ser | Thr | Tyr | Asn | 565 | 570 | 575 | |
| Gln | Lys | Phe | Lys | Asp | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Ser | 580 | 585 | 590 | |
| Thr | Ala | Tyr | Met | Glu | Leu | Leu | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | 595 | 600 | 605 | |
| Tyr | Tyr | Cys | Ala | Arg | Ser | Gly | Tyr | Tyr | Gly | Asp | Ser | Asp | Trp | Tyr | Phe | 610 | 615 | 620 | |
| Asp | Val | Trp | Gly | Ala | Gly | Thr | Thr | Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | 625 | 630 | 635 | 640 |
| Gly | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | Ser | Asp | Ile | Gln | Met | 645 | 650 | 655 | |
| Thr | Gln | Thr | Thr | Ser | Ser | Leu | Ser | Ala | Ser | Leu | Gly | Asp | Arg | Val | Thr | 660 | 665 | 670 | |
| Ile | Ser | Cys | Arg | Ala | Ser | Gln | Asp | Ile | Arg | Asn | Tyr | Leu | Asn | Trp | Tyr | 675 | 680 | 685 | |
| Gln | Gln | Lys | Pro | Asp | Gly | Thr | Val | Lys | Leu | Leu | Ile | Tyr | Tyr | Thr | Ser | 690 | 695 | 700 | |
| Arg | Leu | His | Ser | Gly | Val | Pro | Ser | Lys | Phe | Ser | Gly | Ser | Gly | Ser | Gly | 705 | 710 | 715 | 720 |
| Thr | Asp | Tyr | Ser | Leu | Thr | Ile | Ser | Asn | Leu | Glu | Gln | Glu | Asp | Ile | Ala | 725 | 730 | 735 | |
| Thr | Tyr | Phe | Cys | Gln | Gln | Gly | Asn | Thr | Leu | Pro | Trp | Thr | Phe | Ala | Gly | 740 | 745 | 750 | |
| Gly | Thr | Lys | Leu | Glu | Ile | Lys | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly | 755 | 760 | 765 | |
| Ser | Gly | Gly | Gly | Gly | Ser | Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | 770 | 775 | 780 | |
| Leu | Val | Lys | Pro | Gly | Ala | Ser | Met | Lys | Ile | Ser | Cys | Lys | Ala | Ser | Gly | 785 | 790 | 795 | 800 |
| Tyr | Ser | Phe | Thr | Gly | Tyr | Thr | Met | Asn | Trp | Val | Lys | Gln | Ser | His | Gly | 805 | 810 | 815 | |
| Lys | Asn | Leu | Glu | Trp | Met | Gly | Leu | Ile | Asn | Pro | Tyr | Lys | Gly | Val | Ser | 820 | 825 | 830 | |
| Thr | Tyr | Asn | Gln | Lys | Phe | Lys | Asp | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | 835 | 840 | 845 | |
| Ser | Ser | Ser | Thr | Ala | Tyr | Met | Glu | Leu | Leu | Ser | Leu | Thr | Ser | Glu | Asp | 850 | 855 | 860 | |
| Ser | Ala | Val | Tyr | Tyr | Cys | Ala | Arg | Ser | Gly | Tyr | Tyr | Gly | Asp | Ser | Asp | 865 | 870 | 875 | 880 |
| Trp | Tyr | Phe | Asp | Val | Trp | Gly | Gln | Gly | Thr | Thr | Leu | Thr | Val | Phe | Ser | 885 | 890 | 895 | |

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<210> 17
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature
<222> 15
<223> S = G or C

<400> 17
ggggsggggs ggggs

15

<210> 18
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature
<222> 4,8,12,16
<223> s = g or c

<400> 18
gggsggsgg gsgggs

16

<210> 19
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<221> VARIANT
<222> 2
<223> Xaa= any amino acid

<221> VARIANT
<222> 3
<223> Xaa = s or t

<400> 19
Asn Xaa Xaa
1

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<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

ttggttattg accaaactaa ggctgtccaa

30

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

acctctcttc ttgtttaaga cggagtagat

30

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22

cttgcttttg cggcgcgttt tttttttttt tttttttt

39

<210> 23

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

gataagaatg cggccgccat ttcttggtct ttgggttgaa g

41

<210> 24

<211> 42

<212> DNA

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24

gataagaatg cggccgccaa cttagttgtt gaccagtcta ag

42

<210> 25

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

atagctagca ctttgaagtt cttaattttg ttcctc

36

<210> 26

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26

ataagaatgc ggccgcaagt taatgaaaca ttaagcttac aac

43

<210> 27

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27

gaatgacttg tcctccacc

19

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

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<400> 28
 gaatgacttg tcctccgcgg 20
 <210> 29
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence; note =
 synthetic construct
 <400> 29
 caactagcta gcgctcacia catgaaggtc atgaaattc 39
 <210> 30
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence; note =
 synthetic construct
 <400> 30
 agaaccgtcg agcctattga cgat 24
 <210> 31
 <211> 56
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence; note =
 synthetic construct
 <400> 31
 ccctgcacgc cgatgctatc cacagaagag gaggacaagt cattccaacc atgaag 56
 <210> 32
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence; note =
 synthetic construct
 <400> 32
 gccgatgcta tccacagaag a 21
 <210> 33
 <211> 21

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33

gccgatgcta tccaccgccg c

21

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 34

tctcttcttg ttcaaaacag agtagatacc

30

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<221> misc_feature

<222> 7,15

<223> n = g,a, c or t(u)

<400> 35

gtatgtncac taacntag

18